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GI	Version	Update Date	Status		I	II
14329908	20	Jan 14 2009 11:35 PM		Live	◉	○
14329908	20	May 7 2008 11:09 PM		Dead	○	◉
14329908	20	Feb 27 2008 12:07 AM		Dead	○	○
14329908	20	Jul 11 2007 12:16 AM		Dead	○	○
14329908	20	Jun 29 2007 11:28 PM		Dead	○	○
14329908	20	Jan 19 2007 2:30 PM		Dead	○	○
14329908	20	Oct 17 2006 3:48 PM		Dead	○	○
14329908	20	May 20 2005 12:16 AM		Dead	○	○
14329908	20	Apr 17 2005 12:08 AM		Dead	○	○
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7362702	2	Mar 30 2000 11:14 PM	Dead	○	○
7340634	1	Mar 29 2000 11:12 PM	Dead	○	○

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GI	Version	Update Date	Status	I	II
20545806	6 7	Apr 28 2003 1:32 PM	Suppressed	C	C
20545806	6 7	Apr 10 2003 3:18 PM	Dead	C	C
20545806	6	Jan 5 2003 12:07 AM	Dead	C	C
20545806	6	Aug 1 2002 5:24 PM	Dead	C	C
20545806	6	May 13 2002 4:35 PM	Dead	C	C
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12737962	2	Feb 10 2001 3:10 AM	Dead	C	C
11433661	1	Nov 29 2000 3:54 PM	Dead	C	C

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Search	Most Recent Queries	Time	Result
#8 Search granulocyt* AND (IRS-2 or insulin receptor substrate)		09:41:34	16
#6 Search granulocyt* AND vesnarinone		09:39:32	11
#5 Search Hasegawa K AND granulocyt*		09:38:23	7
#4 Search Hasegawa K		09:38:09	1650
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Clear History

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NCBI Reference Sequence: XM_007095.6

gi|20545806|ref|XM_007095.6|

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Comment Features Sequence

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VERSION     XM_007095.6  GI:20545806
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  ORGANISM  Homo sapiens
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Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1  (bases 1 to 6997)
  AUTHORS   International Human Genome Sequencing Consortium.
  TITLE     The DNA sequence of Homo sapiens
  JOURNAL   Unpublished (2003)
COMMENT     MODEL REFSEQ:  This record is predicted by
automated computational
            analysis. This record is derived from a genomic
sequence
            (NT_009952) annotated using gene prediction
method: BLAST,
            supported by mRNA and EST evidence.
            Also see:
                Documentation of NCBI's Annotation Process

            On May 13, 2002 this sequence version replaced
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XM_007095 (1)   Nucleotide

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proteins. The
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                         abilities to bind inositol phosphates,
and various
                         proteins. PH domains have been found to
possess inserted
                         domains (such as in PLC gamma,
syntrophins) and to be
                         inserted within other domains.
Mutations in Brutons
                         tyrosine kinase (Btk) within its PH
domain cause X-linked
                         agammaglobulinaemia (XLA) in patients.
Point mutations
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of the molecule
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6841 cttccactgt acacgctgta tatagggggtc aatgtgatgc tgctggagac gagaataaac
6901 tggactagaa tagtgcattg tatttagtct gtattgatca tggatgccct ccttaatagc
6961 catatgcaat aaaataaagt acattattta tgaaatg
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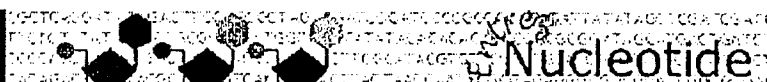
//

All Databases   PubMed   Nucleotide   Protein   Genome   Structure   PMC   Taxonomy   Books

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GenBank: AL162497.20

Human DNA sequence from clone RP11-313L9 on chromosome 13 Contains a novel gene, the IRS2 gene for insulin receptor substrate 2 and two CpG islands, complete sequence

Change Region Shown

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Sequence Analysis Tools

BLAST Sequence

Pick Primers

Comment Features Sequence

```
LOCUS       AL162497               143409 bp    DNA
linear   PRI 13-JAN-2009
DEFINITION  Human DNA sequence from clone RP11-313L9 on
chromosome 13 Contains
            a novel gene, the IRS2 gene for insulin receptor
substrate 2 and
            two CpG islands, complete sequence.
ACCESSION   AL162497
VERSION     AL162497.20  GI:14329908
KEYWORDS    HTG; CpG island; insulin receptor; IRS2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata;
Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates;
Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 143409)
  AUTHORS   Mashreghi-Mohammadi,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2009) Wellcome Trust Sanger
Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
vega@sanger.ac.uk
            Clone requests: Geneservice
(http://www.geneservice.co.uk/) and
            BACPAC Resources (http://bacpac.chori.org/)
COMMENT     On Jun 8, 2001 this sequence version replaced
gi:14280409.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            --------------
            This sequence was finished as follows unless
otherwise noted: all
            regions were either double-stranded or sequenced
with an alternate
            chemistry or covered by high quality data (i.e.,
phred quality >=
            30); an attempt was made to resolve all
sequencing problems, such
            as compressions and repeats; all regions were
covered by at least
            one subclone; and the assembly was confirmed by
```

Homologs of IRS2

The IRS2 gene is conserved in chimpanzee, dog, mouse, rat, chicken, and zebrafish.

Recent Activity

Turn Off   Clear

Human DNA
sequence from clone
AL162497 (1) Nucleotide

metalloproteinase
[Crithidia fasciculata]

162497 (0)   Nucleotide

GenBank.

All links from this record

Assembly

Gene

Gene Genotype

GeneView in dbSNP

Genome Project

Protein

PubMed (Weighted)

Taxonomy

Related Sequences

Map Viewer

OMIM

restriction digest,
          except on the rare occasion of the clone being
a YAC.
          The following abbreviations are used to
associate primary accession
          numbers given in the feature table with their
source databases:
          Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:,
WORMPEP; Information
          on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep
          This sequence was generated from part of
bacterial clone contigs of
          human chromosome 13, constructed by the Sanger
Centre Chromosome 13
          Mapping Group. Further information can be
found at
          http://www.sanger.ac.uk/HGP/Chr13
          IMPORTANT: This sequence is not the entire
insert of clone
          RP11-313L9. It may be shorter because we
sequence overlapping
          sections only once, except for a short overlap.
          During sequence assembly data is compared from
overlapping clones.
          Where differences are found these are
annotated as variations
          together with a note of the overlapping clone
name. Note that the
          variation annotation may not be found in the
sequence submission
          corresponding to the overlapping clone, as we
submit sequences with
          only a small overlap.
          The true right end of clone RP11-358F13 is at
100 in this sequence.
          The true left end of clone RP11-40E6 is at
100074 in this sequence.
          The true right end of clone RP11-313L9 is at
143409 in this
          sequence.
          RP11-313L9 is from the library RPCI-11.2
constructed by the group
          of Pieter de Jong. For further details see
          http://bacpac.chori.org/
          VECTOR: pBACe3.6.
FEATURES   Location/Qualifiers
     source   1..143409
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                     /mol_type="genomic DNA"
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                     /chromosome="13"
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     mRNA   join
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                     /locus_tag="RP11-313L9.1-001"
                     /product="novel transcript"
                     /note="match: ESTs: Em:AW816149.1"
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                     /gene="IRS2"
                     /locus_tag="RP11-313L9.2-001"
     mRNA   complement(join

Genome containing IRS-2 gene

Seq. No. 18

AL162497 (Version 20 Oct. 13, 2002)

XM_0070995

3' ← 5'

mRNA

Ex. 1   4.5kb

Ex. 2   2.4kb

2.6kb

CAT
GTA

~1164   ~2510   4587

31532   29993   15-870

6999

32730bp

143,409b.

126,002b

93,036b